

660	QY	TGTTTCAAGGAAGATTGAACAAATGGCCCTCCCCAACTGTTATCCATTACCTTTCAAG	719
259	Db	TGTTTCAAGGAAGATTGAACAAATGGCCCTCCCCAACTGTTATCCATTACCTTTCAAG	200
720	QY	TCCACCGATGCTATTTTCAAGACATATCCAGTGAATAACAGTGATATGGTTCTTGTTACA	779
199	Db	TCCACCGATGCTATTTTCAAGACATATCCAGTGGATAACAGTGATATGGTTCTTGTTACA	140
780	QY	TGAATGTGTATTTACTCTGTAGGAGATTGTATATTTTAAGTTACCATGATATAAAGTGTGT	839
139	Db	TGAATGTGTATTTACTCTGTAGGAGATTGTATATTTTAAGTTACCATGATATAAAGTGTGT	80
840	QY	AAAAAGGGGGACAGAGAGAAATCTATAAAAAGCCATGTTACTCATGCAATTCGAA	894
79	Db	AAAAAGGGGGACAGAGAGAAATCTATAAAAAGCCATGTTACTCATGCAATTCGAA	25

RESULT 3
 BM272057/c.
 LOCUS
 DEFINITION
 i938e04.y1 HR85 islet Homo sapiens CDNA 5' similar to TR:O9TTK0
 O9TTK0 SER/THR KINASE KKIAMRE. ; mRNA sequence.
 linear EST 20-DEC-2001

BASE COUNT

163 a	120 c	123 g	215 t

ORIGIN

[illegible]

High quality sequence stop: N6.
 Location, Qualifiers
 1. .621

FEATURES
 source

RESULT 4
 AA625895/c

FEATURES
source

TITLE Direct Submission
JOURNAL Submitted (16-JUN-1999) Hiroshi Gomi, The Institute of Physical and Chemical Research (RIKEN), Brain Science Institute (BSI); 2-1 Hironaka, Wako, Saitama 351-0198, Japan
(E-mail: hgom@brain.riken.go.jp, Tel: +81-48-467-9724, Fax: +81-48-467-9725)
FEATURES Location/Qualifiers
1. 3153
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/mol_type="mRNA"
/db_xref="taxon:9986"
/sex="male"
/tissue type="brain"
22. .2022
/note="corresponds to mouse KIAARE-beta"
/cdon_start=1
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/protein_id="BAA88508.1"
/db_xref="GI:6624279"

source

CDS

1. 3153
/organism="Oryctolagus cuniculus"
/mol_type="mRNA"
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/sex="male"
/tissue type="brain"
22. .2022
/note="corresponds to mouse KIAARE-beta"
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BASE COUNT 939 a 577 c 777 g 860 t

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Best Local Similarity 76.7%; Pred. No. 3.5e141;
Matches 1003; Conservative 0; Mismatches 229; Indels 76; Gaps 16;
2 TGGCAATCCCACTACACACATCTTCAGAGTGGATGAGAGAACTAAGAGTGT 121
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62 TGGCAATCCCACTACACACATCTTCAGAGTGGATGAGAGAACTAAGAGTGT 121
1601 TGGCAATCCCACTACACACATCTTCAGAGTGGATGAGAGAACTAAGAGTGT 1657
122 CTATTCATCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181
1658 GTATTCATCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1717
182 CCACATTCATCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
1718 CCACATTCATCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1777
241 CCAG 300
1778 CCAG 1837
301 TGGAGGAG 360
1838 TGGAGGAG 1897
361 CTGAG 420
1898 CTGAG 1957
421 TATGAG 480
1958 TATGAG 2017
481 ACTGAG 558
2018 ACTGAG 2077

533 CTTCAGCAGAGAGTCTGATATCCCAAGAGAGAGAGATTCATGTTTGCATTCCTTC 598
2078 CTTCACCAACAAGCTCTGATATCCCTAGGAGAGAGAGATTCATGTTTGCATTCCTTC 7137
599 TGAATGCTCTGATATTCCTGAGGAGAGCTCTTGAAGAGAGAGAGAGAGAGAGAGAGAG 658
2138 TGAATGCTCTGATATTCCTGAGGAGAGCTCTTGAAGAGAGAGAGAGAGAGAGAGAGAG 2197
659 ATGTTTCAAGAGAGATTCAG 718
2198 ATGTTTCAAGAGAGATTCAG 2256
719 GTCCACCGAGTCTATTCAG 778
2257 GTCCACCGAGTCTATTCAG 2314
779 ATGAATGCTCTGATATTCCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 837
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2568 GAAAG 2627
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2628 ACTGCTGATGTTTGGTCACTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2676
1194 CCACATTCATTCAG 1250
2677 CTACTATGAG 2736
1251 GCATGTTGATTCATCAGTATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1298
2737 ACATT-GAGAGTCTCTGATATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2783

RESULT 4
AR221994
LOCUS AR221994
DEFINITION Sequence 3 from patent US 6428994.
ACCESSION AR221994
VERSION AR221994.1
KEYWORDS GI:23329320
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3080)
AUTHORS Thompson, R.F., Gomi, H. and Sun, W.
TITLE cDNA, genomic, and predicted protein sequences of learning-induced kinases
JOURNAL Patent: US 6428994-A 3 06-AUG-2002;
FEATURES Location/Qualifiers
1. 3080
/organism="unknown"
BASE COUNT 930 a 556 c 751 g 843 t
ORIGIN

Query Match 32.1% Score 624.8; DB 6; Length 3080;
Best Local Similarity 76.5%; Pred. No. 5e-140;
Matches 1000; Conservative 0; Mismatches 232; Indels 76; Gaps 16;

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QY 182 CCACATTAAGTCTCTAGTGAAGAAACCTTCTTGGGCAAGTAAGAAAGAGAGAACT 240
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QY 241 CCAGGACAGATGTCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 300
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QY 301 TGGGAGGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 360
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QY 361 CTCGAATTCCTCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 420
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QY 421 TATCAGGACCTCCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 480
DB TATCAGGACCTCCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1944

QY 481 ACTGAGAACCAATTTTGGTCTCAACTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 538
DB ACTGAGAACCAATTTTGGTCTCAACTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2004

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QY 599 TGAATCGCTGCAATTTCTGAGGAGGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 658
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QY 1076 TTAAGTGA-ATATGTAATCTCTCCATGGGTAGATGTGTATCTTTGA-CTTCTGTAAT 1133
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QY 1251 GCATTGTTAGTTCCTCATGTAATTAAGATCTCTGTCGTCGTCGTCGTCGTCGTCGTC 1298
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RESULT 5

AB029065
LOCUS
DEFINITION
Mus musculus Kkm mRNA for Ser/Thr kinase KKIAMRE-beta, complete cds.
AB029065
ACCESSION
AB029065.1 GI:6594323
VERSION
Ser/Thr kinase KKIAMRE-beta.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 4022)
Sassa, T., Gomi, H., Sun, W., Ikeda, T., Thompson, R.P. and Itohara, S.
The Murine KKIAMRE gene: variants, dual promoters, expression and chromosomal localization
Unpublished
JOURNAL
2 (bases 1 to 4022)
Sassa, T., Gomi, H. and Itohara, S.
Direct Submission
Submitted (16-JUN-1999) Takayuki Sassa, The Institute of Physical and Chemical Research (RIKEN), Brain Science Institute (BSI); 2-1 Hirotsawa, Wako, Saitama 351-0198, Japan
E-mail:tsassa@brain.riken.go.jp, Tel:81-48-467-9724 (ex.7716), Fax:81-48-467-9725

FEATURES

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Location/Qualifiers
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